

SEQUENCE LISTING

<110> Hartley, James L.

Brasch, Michael A.

Temple, Gary F.

Cheo, David

<120> Compositions and Methods for Use in Recombinational
Cloning of Nucleic Acids

<130> 0942.4680003

<140> 09/517,466

<141> 2000-03-02

<150> US 60/122,389

<151> 1999-03-02

<150> US 60/126,049

<151> 1999-03-23

<150> US 60/136,744

<151> 1999-05-28

<160> 285

<170> PatentIn version 3.1

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tcaatttggt gcaacgaaca ggtcactatc agtcaaaata aaatcattat ttg 233

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aatatcaata tattaaatta gattttgcat aaaaaacaga ctacataata ctgtaaaaca	180
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cttgtacaaa gtggt	135

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tgcttttctta taatgccaac tttgtacaag aaagctgggt 100

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22

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primer can have variable length up to maximum of
about 100 kbp; some residues may be missing

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26

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<221> misc_feature

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primer can have variable length up to maximum of
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accactttgt acaagaaagc tgggtn

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primer can have variable length up to maximum of
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about 100 kbp; some residues may be missing

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<210> 27

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aaaagcaggc tn

12

<210> 28

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<221> misc_feature

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<210> 29

<211> 11

<212> DNA

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aaagcaggct n

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<223> attB1 fused into a His6 fusion vector

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1				5					10					15	

Lys	Lys	Ala	Gly	Phe	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Thr	Met
			20					25					30

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Gly	Ile	Thr	Ser	Leu	Tyr	Lys	Lys	Ala	Gly	Phe
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<223> attL Right PCR Primer

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<223> attr2

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<223> attr Right

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<223> B1-Hgb oligonucleotide

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<223> B2-Hgb oligonucleotide

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<223> 18B1-Hgb oligonucleotide

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tgtacaaaaa agcaggct

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<223> 18B2-Hgb oligonucleotide

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tgtacaagaa agctgggt

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<212> DNA

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<223> 15B1-Hgb oligonucleotide

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acaaaaaagc aggct

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<223> 15B2-Hgb oligonucleotide

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<223> 12B2-Hgb oligonucleotide

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gcttttttat actaa

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<210> 70

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<210> 71

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<210> 73

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<210> 75

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<210> 76

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<223> attL5

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<223> ori

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<220>

<221> gene

<222> (324)..(629)

<223> ccdB

<220>

<221> gene

<222> (658)..(757)

<223> attL2

<220>

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<223> ori

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<220>

<221> gene

<222> (655)..(754)

<223> attL2

<220>

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<223> ori

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<211> 2738

<212> DNA

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<220>

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<222> (676)..(775)

<223> attL2

<220>

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<223> KmR

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<221> gene

<222> (1812) .. (2385)

<223> ori

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<211> 2735

<212> DNA

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<220>

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<222> (673) .. (772)

<223> attL2

<220>

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<222> (895) .. (1704)

<223> KmR

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<222> (1809) .. (2382)

<223> ori

<400> 125

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<223> pENTR2B multiple cloning site

<400> 189

Leu	Tyr	Lys	Lys	Ala	Gly	Trp	Arg	Arg	Asn	Gln	Phe	Ser	Arg	Leu	Asp
1				5					10					15	

Pro	Val	Pro	Asn
			20

<210> 190

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 190

g	aat	tcg	cgg	ccg	cac	tcg	aga	tat	cta	gac	cca	gct	ttc	ttg	tac	aaa	49
	Asn	Ser	Arg	Pro	His	Ser	Arg	Tyr	Leu	Asp	Pro	Ala	Phe	Leu	Tyr	Lys	
1					5					10					15		

g																	50
---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	----

<210> 191

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR2B multiple cloning site

<400> 191

Asn	Ser	Arg	Pro	His	Ser	Arg	Tyr	Leu	Asp	Pro	Ala	Phe	Leu	Tyr	Lys
1				5					10					15	

<210> 192

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

<400> 192

ttg	tac	aaa	aaa	gca	ggc	tct	tta	aag	gaa	cca	att	cag	tcg	act	gga	48
Leu	Tyr	Lys	Lys	Ala	Gly	Ser	Leu	Lys	Glu	Pro	Ile	Gln	Ser	Thr	Gly	
1				5					10					15		

tcc	ggt	acc	gaa	ttc	gatcgc	69
Ser	Gly	Thr	Glu	Phe		
			20			

<210> 193

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<400> 193

Leu Tyr Lys Lys Ala Gly Ser Leu Lys Glu Pro Ile Gln Ser Thr Gly
1 5 10 15

Ser Gly Thr Glu Phe
20

<210> 194

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 194

g aat tcg cgg ccg cac tcg aga tat cta gac cca gct ttc ttg tac aaa 49
Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

g 50

<210> 195

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR3C multiple cloning site

<400> 195

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

<210> 196

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

<400> 196

ttg	tac	aaa	aaa	gca	ggc	tcc	acc	atg	gga	acc	aat	tca	gtc	gac	tgg	48
Leu	Tyr	Lys	Lys	Ala	Gly	Ser	Thr	Met	Gly	Thr	Asn	Ser	Val	Asp	Trp	
1				5					10					15		

atc	cgg	tac	cga	att	c	64
Ile	Arg	Tyr	Arg	Ile		
			20			

<210> 197

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<400> 197

Leu	Tyr	Lys	Lys	Ala	Gly	Ser	Thr	Met	Gly	Thr	Asn	Ser	Val	Asp	Trp
1				5					10					15	

Ile	Arg	Tyr	Arg	Ile
			20	

<210> 198

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 198

g aat tcg cgg ccg cac tcg aga tat cta gac cca gct ttc ttg tac aaa 49

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

g 50

<210> 199

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR4 multiple cloning site

<400> 199

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

<210> 200

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR5 multiple cloning site

<220>

<221> CDS

<222> (1)..(63)

<223>

<400> 200

ttg	tac	aaa	aaa	gca	ggc	ttt	cat	atg	gga	acc	aat	tca	gtc	gac	tgg	48
Leu	Tyr	Lys	Lys	Ala	Gly	Phe	His	Met	Gly	Thr	Asn	Ser	Val	Asp	Trp	
1				5					10					15		

atc	cgg	tac	cga	att	cgc	66
Ile	Arg	Tyr	Arg	Ile		
			20			

<210> 201

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR5 multiple cloning site

<400> 201

Leu	Tyr	Lys	Lys	Ala	Gly	Phe	His	Met	Gly	Thr	Asn	Ser	Val	Asp	Trp
1				5					10					15	

Ile	Arg	Tyr	Arg	Ile
			20	

<210> 202

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR5 multiple cloning site

<400> 202

agaattcgcg	gccgcactcg	agatatctag	accagcttt	cttgtacaaa	g	51
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<210> 203

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR6 multiple cloning site

<220>

<221> CDS

<222> (1)..(60)

<223>

<400> 203

ttg	tac	aaa	aaa	gca	ggc	tgc	atg	cga	acc	aat	tca	gtc	gac	tgg	atc	48
Leu	Tyr	Lys	Lys	Ala	Gly	Cys	Met	Arg	Thr	Asn	Ser	Val	Asp	Trp	Ile	
1				5					10					15		

cgg	tac	cga	att	cgc												63
Arg	Tyr	Arg	Ile													
			20													

<210> 204

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR6 multiple cloning site

<400> 204

Leu	Tyr	Lys	Lys	Ala	Gly	Cys	Met	Arg	Thr	Asn	Ser	Val	Asp	Trp	Ile	
1				5					10					15		

Arg	Tyr	Arg	Ile													
			20													

<210> 205

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR6 multiple cloning site

<400> 205

agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g

51

<210> 206

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR7 multiple cloning site

<220>

<221> CDS

<222> (1)..(81)

<223>

<400> 206

ttg tac aaa aaa gca ggc ttt gaa aac ctg tat ttt caa gga acc gtt
Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Val
1 5 10 15

48

tca tgc atc gtc gac tgg atc cgg tac cga att cgc
Ser Cys Ile Val Asp Trp Ile Arg Tyr Arg Ile
20 25

84

<210> 207

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR7 multiple cloning site

<400> 207

Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Val
1 5 10 15

Ser Cys Ile Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 208

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR7 multiple cloning site

<400> 208
agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g 51

<210> 209

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR8 multiple cloning site

<220>

<221> CDS

<222> (1) .. (78)

<223>

<400> 209
ttg tac aaa aaa gca ggc ttt gaa aac ctg tat ttt caa gga acc atg 48
Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Met
1 5 10 15

gac cta gtc gac tgg atc cgg tac cga att cgc 81
Asp Leu Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 210

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR8 multiple cloning site

<400> 210

Leu	Tyr	Lys	Lys	Ala	Gly	Phe	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Thr	Met
1				5					10					15	

Asp	Leu	Val	Asp	Trp	Ile	Arg	Tyr	Arg	Ile
			20					25	

<210> 211

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR8 multiple cloning site

<400> 211

agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g

51

<210> 212

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR9 multiple cloning site

<220>

<221> CDS

<222> (1)..(78)

<223>

<400> 212
ttg tac aaa aaa gca ggc ttt gaa aac ctg tat ttt caa gga cat atg 48
Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly His Met
1 5 10 15

aga tct gtc gac tgg atc cgg tac cga att cgc 81
Arg Ser Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 213

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR9 multiple cloning site

<400> 213

Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly His Met
1 5 10 15

Arg Ser Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 214

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR9 multiple cloning site

<400> 214
agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g 51

<210> 215

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<220>

<221> CDS

<222> (1)..(81)

<223>

<400> 215
ttg tac aaa aaa gca ggc ttc gaa cta agg aaa tac tta cat atg gga 48
Leu Tyr Lys Lys Ala Gly Phe Glu Leu Arg Lys Tyr Leu His Met Gly
1 5 10 15

acc aat tca gtc gac tgg atc cgg tac cga att cgc 84
Thr Asn Ser Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 216

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<400> 216

Leu Tyr Lys Lys Ala Gly Phe Glu Leu Arg Lys Tyr Leu His Met Gly
1 5 10 15

Thr Asn Ser Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 217

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR10 multiple cloning site

<400> 217

agaattcgcg gccgcactcg agatatctag acccagcttt cttgtacaaa g

51

<210> 218

<211> 88

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<220>

<221> CDS

<222> (1)..(87)

<223>

<400> 218

ttg tac aaa aaa gca ggc ttc gaa gga gat aga acc aat tct cta agg
Leu Tyr Lys Lys Ala Gly Phe Glu Gly Asp Arg Thr Asn Ser Leu Arg
1 5 10 15

48

aaa tac tta acc atg gtc gac tgg atc cgg tac cga att c
Lys Tyr Leu Thr Met Val Asp Trp Ile Arg Tyr Arg Ile
20 25

88

<210> 219

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<400> 219

Leu Tyr Lys Lys Ala Gly Phe Glu Gly Asp Arg Thr Asn Ser Leu Arg
1 5 10 15

Lys Tyr Leu Thr Met Val Asp Trp Ile Arg Tyr Arg Ile
20 25

<210> 220

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<220>

<221> CDS

<222> (2)..(49)

<223>

<400> 220

g aat tcg cgg ccg cac tcg aga tat cta gac cca gct ttc ttg tac aaa 49
Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

g 50

<210> 221

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pENTR11 multiple cloning site

<400> 221

Asn Ser Arg Pro His Ser Arg Tyr Leu Asp Pro Ala Phe Leu Tyr Lys
1 5 10 15

<210> 222

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST1

<400> 222

atgagctggt gacaattaat catccggctc gtataatgtg tggaattgtg agcggataac 60

aatttcacac aggaaacaga caggtatagg atcacaagtt tgtacaaaaa agctgaacga 120

<210> 223

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST2

<220>

<221> CDS

<222> (94)..(135)

<223>

<400> 223

aatattctga aatgagctgt tgacaattaa tcatccggctc cgtataatct gtggaattgt 60

gagcggataa caatttcaca caggaaacag acc atg tcg tac tac cat cac cat 114
Met Ser Tyr Tyr His His His
1 5

cac cat cac ggc atc aca agt ttgtacaaaa aagctgaa 153
His His His Gly Ile Thr Ser
10

<210> 224

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST2

<400> 224

Met	Ser	Tyr	Tyr	His	His	His	His	His	His	Gly	Ile	Thr	Ser
1				5					10				

<210> 225

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST3

<220>

<221> CDS

<222> (106)..(120)

<223>

<400> 225

cggttctggc	aaatattctg	aatgagctg	ttgacaatta	atcatcggct	cgtataatgt	60
------------	------------	-----------	------------	------------	------------	----

gtggaattgt	gagcggataa	caatttcaca	caggaaacag	tattc	atg	tcc	cct	ata	117
					Met	Ser	Pro	Ile	
					1				

cta	ggttattgga	aaattaaggg	ccttgtgcaa	ccc	153
Leu					
5					

<210> 226

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST3

<400> 226

Met	Ser	Pro	Ile	Leu
1				5

<210> 227
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> pDEST3
<220>
<221> CDS
<222> (10)..(63)
<223>

<400> 227
ctgggttcg cgt gga tct cgt cgt gca tct gtt gga tcc cca tca aca agt 51
Arg Gly Ser Arg Arg Ala Ser Val Gly Ser Pro Ser Thr Ser
1 5 10

ttg tac aaa aaa gctgaacgag aaacgtaaaa tgatataaat atcaatata 102
Leu Tyr Lys Lys
15

<210> 228
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> pDEST3
<400> 228
Arg Gly Ser Arg Arg Ala Ser Val Gly Ser Pro Ser Thr Ser Leu Tyr
1 5 10 15

Lys Lys

<210> 229
<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST4

<220>

<221> CDS

<222> (97)..(246)

<223>

<400> 229

gcaaataattc tgaaatgagc tgttgacaat taatcatccg gtccgtataa tctgtggaat 60

tgtgagcggg taacaatttc acacaggaaa cagacc atg ggt cat cat cat cat 114
Met Gly His His His His
1 5

cat cac gat tac gat atc cca acg acc gaa aac ctg tat ttt cag ggc 162
His His Asp Tyr Asp Ile Pro Thr Thr Glu Asn Leu Tyr Phe Gln Gly
10 15 20

gcc cat atg agc gat aaa att att cac ctg act gac gac agt gat gac 210
Ala His Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Asp Asp
25 30 35

gat gac aag gta ccc atc aca agt ttg tac aaa aaa gctgaacga 255
Asp Asp Lys Val Pro Ile Thr Ser Leu Tyr Lys Lys
40 45 50

<210> 230

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST4

<400> 230

Met Gly His His His His His His Asp Tyr Asp Ile Pro Thr Thr Glu
1 5 10 15

Asn Leu Tyr Phe Gln Gly Ala His Met Ser Asp Lys Ile Ile His Leu
20 25 30

Thr Asp Asp Ser Asp Asp Asp Asp Lys Val Pro Ile Thr Ser Leu Tyr
 35 40 45

Lys Lys
 50

<210> 231

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST5

<400> 231
 aggcacccca ggctttacac tttatgcttc cggctcgtat gttgtgtgga attgtgagcg 60
 gataacaatt tcacacagga aacagctatg accatgatta cgccaagctc taatacgact 120
 cactataggg aaagctggta cgcctgcagg taccgggtccg gaattcccgg gtcgacgac 180
 acaagtttgt acaaaaaagc tgaa 204

<210> 232

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST5

<400> 232
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 agaggatcca agcttacgta cgcgtgcatg cgacgtcata gctcttctat agtgtcacct 120
 aaattcaatt cactggccgt cgttttataa cgtcgtgact gggaaaaccc tggcgttacc 180
 caacttaatc gccttgcagc acat 204

<210> 233

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST6

<400> 233

taacgccagg gttttcccag tcacgacggt gtaaaacgac ggccagtga ttgaatttag	60
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagcttg gacccctctag	120
agcggccgcc gactagtgat cacaagtttg taaaaaaaag ctgaacgaga aacgtaaaat	180
gatataaata tcaatatatt aaat	204

<210> 234

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST6

<400> 234

tatttatatc attttacggt tctcggttcag ctttcttgta caaagtgggtg atcgtcgacc	60
cgggaattcc ggaccgggtac ctgcaggcgt accagctttc cctatagtga gtcgtattag	120
agcttggcgt aatcatgggtc atagctgttt cctgtgtgaa attgttatcc gtcacaatt	180
ccacacaaca tacgagccgg aagcataaag tgtaaagcct ggggtgccta atgagtgagc	240
taactcacat taatt	255

<210> 235

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST7

<400> 235

ccattgacgc aaatgggcgg taggcgtgta cggtgggagg tctatataag cagagctcgt	60
ttagtgaacc gtcagatcgc ctggagacgc catccacgct gttttgacct ccatagaaga	120

caccgggacc gatccagcct ccggactcta gcctaggccg cggagcggat aacaatttca	180
cacaggaaac agctatgacc actaggcttt tgcaaaaagc tatttaggtg acactataga	240
aggtagcct gcaggtaccg gtccggaatt cccatcacaa gtttgtacaa aaaagctgaa	300
cgagaa	306

<210> 236

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST8

<400> 236

cgtatactcc ggaatattaa tagatcatgg agataattaa aatgataacc atctcgcaaa	60
taaataagta ttttactgtt ttcgtaacag ttttgtaata aaaaaaccta taaatattcc	120
ggattattca taccgtccca ccacggggcg cggatcatca caagtttgta caaaaaagct	180
gaacgagaaa cgtaaaatga tata	204

<210> 237

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST9

<400> 237

ttggcgaggg acattaaggc gtttaagaaa ttgagaggac ctgttataca cctctacggc	60
ggtcctagat tgggtgcgtta atacacagaa ttctgattgg atcccgggtcc gaagcgcgct	120
ttcccatcaa caagtttgta caaaaaagct gaa	153

<210> 238

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST10

<220>

<221> CDS

<222> (109)..(201)

<223>

<400> 238

aaataagtat tttactgttt tcgtaacagt tttgtaataa aaaaacctat aaatattccg 60

gattattcat accgtcccac catcgggcgc ggatctcggt ccgaaacc atg tcg tac 117
Met Ser Tyr
1

tac cat cac cat cac cat cac gat tac gat atc cca acg acc gaa aac 165
Tyr His His His His His His Asp Tyr Asp Ile Pro Thr Thr Glu Asn
5 10 15

ctg tat ttt cag ggc atc aca agt ttg tac aaa aaa gct 204
Leu Tyr Phe Gln Gly Ile Thr Ser Leu Tyr Lys Lys
20 25 30

<210> 239

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST10

<400> 239

Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
1 5 10 15

Thr Glu Asn Leu Tyr Phe Gln Gly Ile Thr Ser Leu Tyr Lys Lys
20 25 30

<210> 240

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST11

<400> 240

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tagtgaaccg tcagatcgcc tggagacgcc atccacgctg ttttgacctc catagaagac      60
accgggaccg atccagcctc cgcggccccc aattcgagct cggtagcccg ggatcctcta      120
gagtcgaggt cgacgggtatc gataagcttg atatcaacaa gtttgtacaa aaaagctgaa      180
cgagaaacgt aaaatgatat aaat                                             204
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<210> 241

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST12.2

<400> 241

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accgtcagat cgcctggaga cgccatccac gctgttttga cctccataga agacaccggg      60
accgatccag cctccggact ctagcctagg ccgcggagcg gataacaatt tcacacagga      120
aacagctatg accattaggc ctttgcaaaa agctatttag gtgacactat agaaggtagc      180
cctgcaggta ccggtccgga attcccatca acaagtttgt acaaaaaagc tgaacgagaa      240
acgtaaaatg atata                                                         255
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<210> 242

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST13

<400> 242

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tgggcaaacc aagacagcta aagatctctc acctaccaa caatgcccc ctgcaaaaaa      60
taaattcata taaaaaacat acagataacc atctgcggtg ataaattatc tctggcggtg      120
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ttgacataaa taccactggc ggtgatactg agcacatcag caggacgcac tgaccaccat 180
gaaggtgacg ctcttaaaaa ttaagccctg aagaagggca gcattcaaag cagaaggctt 240
tgggggtgtgt gatacgaaac gaagcattgg gatcatcaca agtttgtaca aaaaagctga 300

<210> 243

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST14

<400> 243

tgccggccac gatgcgtccg gcgtagagga tcgagatctc gatcccgcga aattaatacg 60
actcactata gggagaccac aacgggtttcc ctctagatca caagtttgta caaaaaagct 120

<210> 244

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST15

<220>

<221> misc_feature

<222> (1)..(1)

<223> 'n' can be any nucleotide (A, T, C, G or U)

<220>

<221> CDS

<222> (106)..(120)

<223>

<400> 244

natcgagatc tcgatcccgcc gaaattaata cgactcacta tagggagacc acaacgggttt 60
ccctctagaa ataattttgt ttaactttaa gaaggagata tacat atg tcc cct ata 117
Met Ser Pro Ile
1
cta gggtattgga aaattaaggg ccttggtgcaa ccactcgac ttcttttgga 170
Leu
5
atatcttgaa gaaaaatatg aagagcattt gtat 204

<210> 245

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST15

<220>

<221> misc_feature

<222> (1)..(1)

<223> may be any nucleotide

<400> 245

Met Ser Pro Ile Leu
1 5

<210> 246

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST15

<220>

<221> CDS

<222> (70)..(99)

<223>

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<400> 246
cagggctggc aagccacgtt tgggtgggtggc gaccatcctc caaaatcgga tctgggttccg      60
cgtccatgg tcg aat caa aca agt ttg tac aaa aaa gct gaacgagaaa      109
      Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
      1              5              10

cgtaaaatga tataaatatc aatatattaa attagatttt gcat      153

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<210> 247

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST15

<400> 247

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Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1              5              10

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<210> 248

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<220>

<221> CDS

<222> (100)..(111)

<223>

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<400> 248
gatctcgatc ccgcgaaatt aatacgactc actataggga gaccacaacg gtttcctct      60
agaaataatt ttgtttaact ttaagaagga gatatacat atg agc gat aaa      111
      Met Ser Asp Lys
      1

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attattcacc tgactgacga cagttttgac acggatgtac tc 153

<210> 249

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<400> 249

Met Ser Asp Lys
1

<210> 250

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<220>

<221> CDS

<222> (82) .. (123)

<223>

<400> 250

gtggcggcaa ccaaagtggg tgcactgtct aaaggtcagt tgaaagagtt cctcgacgct 60

aacctggccg gttctgggttc t ggt gat gac gat gac aag atc aca agt ttg 111
Gly Asp Asp Asp Asp Lys Ile Thr Ser Leu
1 5 10

tac aaa aaa gct gaacgagaaa cgtaaaatga tataaatatc 153
Tyr Lys Lys Ala

<210> 251

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST16 multiple cloning site

<400> 251

Gly	Asp	Asp	Asp	Asp	Lys	Ile	Thr	Ser	Leu	Tyr	Lys	Lys	Ala
1				5					10				

<210> 252

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST17 multiple cloning site

<220>

<221> CDS

<222> (94)..(153)

<223>

<400> 252

gatccccgcga	aattaatacg	actcactata	gggagaccac	aacgggtttcc	ctctagaaat	60
-------------	------------	------------	------------	-------------	------------	----

aattttgttt	aactttaaga	aggagatata	cat	atg	tcg	tac	tac	cat	cac	cat	114
				Met	Ser	Tyr	Tyr	His	His	His	
				1				5			

cac	cat	cac	ctc	gaa	tca	aca	agt	ttg	tac	aaa	aaa	gct	153
His	His	His	Leu	Glu	Ser	Thr	Ser	Leu	Tyr	Lys	Lys	Ala	
		10					15					20	

<210> 253

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST17 multiple cloning site

<400> 253

Met	Ser	Tyr	Tyr	His	His	His	His	His	His	Leu	Glu	Ser	Thr	Ser	Leu
1				5					10					15	

Tyr	Lys	Lys	Ala
			20

<210> 254

<211> 420

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST18 p10 Promoter

<400> 254

gaagacctcg gccgtcgagg cgcttgccgg tgggtgctgac cccggatgaa gtgggttcgca	60
tcctcgggttt tctggaaggc gagcatcggt tgttcgccca ggactctagc tatagttcta	120
gtgggttggt acgtatcgag caagaaaata aaacgccaaa cgcgttggag tcttgtgtgc	180
tattttttaca aagattcaga aatacgcac acttacaaca aggggggacta tgaaattatg	240
cattttgagg atgccgggac ctttaattca acccaacaca atatattata gttaaataag	300
aattatttat caaatcattt gtatattaat taaaatacta tactgtaaat tacattttat	360
ttacaatgag gatcatcaca agtttgtaca aaaaagctga acgagaaacg taaaatgata	420

<210> 255

<211> 300

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST19 39K Promoter

<400> 255

ggtgacgccg tcattctttcc attgtaacgt aaatggcaac ttgtagatga acgcgctgtc	60
aaaaaaccgg ccagtttctt ccacaaactc gcgcacgggt gtctcgtaaa cttttgcgtc	120

```

gcaacaatcg cgatgacctc gtggtatgga aattttttct aaaaaagtgt cgttcatgtc 180
ggcggcgggcg ttcgcgctcc ggtacgcgcg acgggcacac agcaggacag ccttgtccgg 240
ctcgattatc ataaacaatc ctgcaggcat gcaagctgga tcatcacaag tttgtacaaa 300

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<210> 256

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<220>

<221> CDS

<222> (163)..(174)

<223>

<400> 256

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ggctacgtat actccggaat attaatagat catggagata attaaaatga taaccatctc 60
gcaaataaat aagtatttta ctgttttcgt aacagttttg taataaaaaa acctataaat 120
attccggatt attcataccg tcccaccatc gggcgcggat cc atg gcc cct ata 174
                                         Met Ala Pro Ile
                                         1
ctaggttatt ggaaaattaa gggccttgtg 204

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<210> 257

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<400> 257

Met Ala Pro Ile

1

<210> 258

<211> 95

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<220>

<221> CDS

<222> (1)..(48)

<223>

<400> 258

tcg gat ctg gtt ccg cgt cat aat caa aca agt ttg tac aaa aaa gct	48
Ser Asp Leu Val Pro Arg His Asn Gln Thr Ser Leu Tyr Lys Lys Ala	
1 5 10 15	

gaacgagaaa cgtaaaatga tataaatatc aatatattaa attagat	95
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<210> 259

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST20 Polyhedron Promoter

<400> 259

Ser Asp Leu Val Pro Arg His Asn Gln Thr Ser Leu Tyr Lys Lys Ala	
1 5 10 15	

<210> 260

<211> 204

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST21 Promoter region

<220>

<221> CDS

<222> (163)..(180)

<223>

<400> 260

ttgccgcttt gctatcaagt ataaatagac ctgcaattat taatcttttg tttcctcgtc 60

attgttctcg tttcctttct tcttgtttc tttttctgca caatatttca agctatacca 120

agcatacaat caactccaag cttgaagcaa gcctcctgaa ag atg aag cta ctg 174

Met Lys Leu Leu
1

tct tct atcgaacaag catgcatat ttgc 204

Ser Ser

5

<210> 261

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST21 Promoter region

<400> 261

Met Lys Leu Leu Ser Ser

1 5

<210> 262

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST21 Promoter region

<220>

<221> CDS

<222> (37)..(78)

<223>

<400> 262

gaagagagta	gtaacaaagg	tcaaagacag	ttgact	gta	tcg	tcg	agg	tcg	aat	54
				Val	Ser	Ser	Arg	Ser	Asn	
				1				5		

caa	aca	agt	ttg	tac	aaa	aaa	gct	gaacgagaaa	cgtaaaatga	tata	102
Gln	Thr	Ser	Leu	Tyr	Lys	Lys	Ala				
			10								

<210> 263

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST21 Promoter region

<400> 263

Val	Ser	Ser	Arg	Ser	Asn	Gln	Thr	Ser	Leu	Tyr	Lys	Lys	Ala
1				5					10				

<210> 264

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST22 Promoter region

<220>

<221> CDS

<222> (217)..(228)

<223>

<400> 264
acgcacacta ctctctaatag agcaacggta tacggccttc cttccagtta cttgaatttg 60
aaataaaaaa agtttgccgc tttgctatca agtataaata gacctgcaat tattaatctt 120
ttgtttcctc gtcattgttc tcgttcctt tcttccttgt ttctttttct gcacaatatt 180
tcaagctata ccaagcatac aatcaactcc aagctt atg ccc aag aag 228
Met Pro Lys Lys
1
aagcgggaagg tctcgagcgg cgccaat 255

<210> 265
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> pDEST22 Promoter region
<400> 265
Met Pro Lys Lys
1

<210> 266
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> pDEST22
<220>
<221> CDS
<222> (28) .. (66)
<223>

<400> 266
gaagatacc caccaaaccc aaaaaaa gag ggt ggg tcg aat caa aca agt ttg 54
Glu Gly Gly Ser Asn Gln Thr Ser Leu

1

5

tac aaa aaa gct gaacgagaaa cgtaaa
Tyr Lys Lys Ala
10

82

<210> 267

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST22

<400> 267

Glu Gly Gly Ser Asn Gln Thr Ser Leu Tyr Lys Lys Ala
1 5 10

<210> 268

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<400> 268

atcccgcgaa attaatacga ctactatag ggagaccaca acggtttccc tctagatcac 60

aagtttgtac aaaaaagctg aacgagaaac gtaaaatgat at 102

<210> 269

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<220>

<221> CDS

<222> (61)..(126)

<223>

<400> 269

tttttatgca aaatctaatt taatatattg atatttatat cattttacgt ttctcgttca 60

gct ttc ttg tac aaa gtg gtg att atg tcg tac tac cat cac cat cac 108
Ala Phe Leu Tyr Lys Val Val Ile Met Ser Tyr Tyr His His His His
1 5 10 15

cat cac ctc gat gag caa taactagcat aacccttgg ggcctct 153
His His Leu Asp Glu Gln
20

<210> 270

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST23 T7 promoter

<400> 270

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Tyr Tyr His His His His
1 5 10 15

His His Leu Asp Glu Gln
20

<210> 271

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST24 T7 promoter

<400> 271

atcgagatct cgatcccgcg aaattaatac gactcactat agggagacca caacggtttc 60

cctctagatc acaagtttgt acaaaaaagc tgaacgagaa ac 102

<210> 272
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> pDEST24 T7 promoter
<220>
<221> CDS
<222> (22)..(60)
<223>

<400> 272
tcattttacg tttctcgttc a gct ttc ttg tac aaa gtg gtg att atg tcc 51
Ala Phe Leu Tyr Lys Val Val Ile Met Ser
1 5 10

cct ata cta ggttattgga aaattaaggg ccttgtgcaa ccactcgac tt 102
Pro Ile Leu

<210> 273
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> pDEST24 T7 promoter
<400> 273
Ala Phe Leu Tyr Lys Val Val Ile Met Ser Pro Ile Leu
1 5 10

<210> 274
<211> 102
<212> DNA
<213> Artificial Sequence

<220>

<223> pDEST25 T7 promoter

<220>

<221> misc_feature

<222> (1)..(1)

<223> 'n' can be any nucleotide (A, T, C, G or U)

<400> 274

nagatctcga tcccgcgaaa ttaatacgac tcactatagg gagaccacaa cggtttcct 60

ctagatcaca agtttgtaga aaaaagctga acgagaaacg ta 102

<210> 275

<211> 102

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST25 T7 promoter

<220>

<221> CDS

<222> (19)..(60)

<223>

<400> 275

ttttacgttt ctcgttca gct ttc ttg tac aaa gtg gtg att atg agc gat 51

Ala Phe Leu Tyr Lys Val Val Ile Met Ser Asp
1 5 10

aaa att att cacctgactg acgacagttt tgacacggat gtactcaaag cg 102

Lys Ile Ile

<210> 276

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST25 T7 promoter

<400> 276

Ala	Phe	Leu	Tyr	Lys	Val	Val	Ile	Met	Ser	Asp	Lys	Ile	Ile
1				5				10					

<210> 277

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST26 CMV promoter

<220>

<221> CDS

<222> (238)..(297)

<223>

<400> 277

ttgacgtcaa	tgggagtttg	ttttggcacc	aaaatcaacg	ggactttcca	aaatgtcgta	60
acaactccgc	cccattgacg	caaatgggcg	gtaggcgtgt	acggtgggag	gtctatataa	120
gcagagctcg	tttagtgaac	cgtcagatcg	cctggagacg	ccatccacgc	tgttttgacc	180
tccatagaag	acaccgggac	cgatccagcc	tccggactct	agcctaggcc	gcggacc	237
atg gcg tac tac	cat cac cat	cac cat cac	tct aga tca	aca agt ttg		285
Met Ala Tyr Tyr	His His His	His His His	Ser Arg Ser	Thr Ser Leu		
1	5	10		15		
tac aaa aaa	gct gaacgagaa					306
Tyr Lys Lys	Ala					
	20					

<210> 278

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST26 CMV promoter

<400> 278

Met	Ala	Tyr	Tyr	His	His	His	His	His	His	Ser	Arg	Ser	Thr	Ser	Leu
1				5					10					15	

Tyr	Lys	Lys	Ala
			20

<210> 279

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST27 promoter

<220>

<221> misc_feature

<222> (1)..(1)

<223> 'n' can be any nucleotide (A, T, C, G or U)

<220>

<221> CDS

<222> (139)..(153)

<223>

<400> 279

nacggtggga	ggtctatata	agcagagctc	gtttagtga	ccgtcagatc	gcctggagac	60
gccatccacg	ctgttttgac	ctccatagaa	gacaccggga	ccgatccagc	ctccggactc	120
tagcctaggc	cgcggacc	atg gcc cct	ata cta	ggttattgga	aaattaaggg	173
		Met Ala Pro	Ile Leu			
		1	5			
ccttggtgcaa	cccactcgac	ttcttttgga	atatcttgaa	gaaaaatatg	aagagcattt	233

gtatgagcgc gatgaaggtg at

255

<210> 280

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> pDEST27 promoter

<220>

<221> misc_feature

<222> (1)..(1)

<223> 'n' can be any nucleotide (A, T, C, G or U)

<400> 280

Met Ala Pro Ile Leu
1 5

<210> 281

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> pDEST27 promoter

<220>

<221> CDS

<222> (37)..(75)

<223>

<400> 281

tttgggtgggtg gcgaccatcc tccaaaatcg gatctg gtt ccg cgt tct aga tca 54
Val Pro Arg Ser Arg Ser
1 5

aca agt ttg tac aaa aaa gct gaacgagaaa cg 87
Thr Ser Leu Tyr Lys Lys Ala

10

<210> 282
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> pDEST27 promoter
<400> 282

Val	Pro	Arg	Ser	Arg	Ser	Thr	Ser	Leu	Tyr	Lys	Lys	Ala
1				5					10			

<210> 283
<211> 405
<212> DNA
<213> Artificial Sequence

<220>
<223> pEXP501

<400> 283
agagctcggt tagtgaaccg tcagatcgcc tggagacgcc atccacgctg ttttgacctc 60
catagaagac accgggaccg atccagcctc cggactctag cctaggccgc ggagcggata 120
acaatttcac acaggaaaca gctatgacca ttaggcctat ttaggtgaca ctatagaaca 180
agtttgtaca aaaaagcagg ctggtaccgg tccggaattc ccgggatatc gtcgacgagc 240
tcactagtcg gcggccgctc tagagtatcc ctcgaggggc ccaagcttac gcgtacccag 300
ctttcttgta caaagtggtc cctatagtga gtcgtattat aagctaggca ctggccgctc 360
ttttacaacg tcgtgactgg gaaaactgct agcttgggat ctttg 405

<210> 284
<211> 153
<212> DNA
<213> Artificial Sequence

$\langle 220 \rangle$

<223> His6-CAT

 $\langle 220 \rangle$

<221> CDS

<222> (31) .. (153)

<223>

<400> 284

cggataacaa tttcacacag gaaacagacc atg tcg tac tac cat cac cat cac 54
Met Ser Tyr Tyr His His His His
1 5

cat cac ggc atc aca agt ttg tac aaa aaa gca ggc ttt gaa aac ctg 102
His His Gly Ile Thr Ser Leu Tyr Lys Lys Ala Gly Phe Glu Asn Leu
10 15 20

tat	ttt	caa	gga	acc	atg	gag	aaa	aaa	atc	act	gga	tat	acc	acc	gtt	150
Tyr	Phe	Gln	Gly	Thr	Met	Glu	Lys	Lys	Ile	Thr	Gly	Tyr	Thr	Thr	Val	
25					30					35					40	

gat	153
Asp	

<210> 285

<211> 41

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> His6-CAT

<400> 285

Met Ser Tyr Tyr His His His His His His Gly Ile Thr Ser Leu Tyr
1 5 10 15

Lys Lys Ala Gly Phe Glu Asn Leu Tyr Phe Gln Gly Thr Met Glu Lys
20 25 30

Lys Ile Thr Gly Tyr Thr Thr Val Asp
35 40